

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS. PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO-REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
- Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

## Raw Sequence Listing Error Summary

RROR DETECTED	SUGGESTED CORRECTION SERIAL NUMBER: _/O/7/3,578
TTN: NEW RULES CASES:	PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE
IWrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
3Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
4Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5Variable Length	Sequence(s)contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6Patentin 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
7Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  This sequence is intentionally skipped
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
8Skipped Sequences (NEW RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
9Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing.  Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
10Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11Use of <220>	Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of Patentln version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13 Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



**IFWO** 

RAW SEQUENCE LISTING

DATE: 01/03/2005

PATENT APPLICATION: US/10/713,578

TIME: 15:44:38

Input Set : A:\124263-1006 SEQUENCE LISTING.ST25.txt

Output Set: N:\CRF4\01032005\J713578.raw

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3 <110> APPLICANT: Awasthi, Sanjay
         Singhal, Sharad S.
 6 <120> TITLE OF INVENTION: Liposomes For Protection Against Toxic Compounds
 8 <130> FILE REFERENCE: 124263-1006
10 <140> CURRENT APPLICATION NUMBER: US 10/713,578
11 <141> CURRENT FILING DATE: 2003-11-13
13 <150> PRIOR APPLICATION NUMBER: 60/425,814
14 <151> PRIOR FILING DATE: 2002-11-13
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 655in VA
22 <212> TYPE: PRT
23 <213> ORGANISM: (recombinant
25 <4.00> SEQUENCE: 1
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35 Ile Ser Pro Thr Lys Phe Pro Gly Leu Tyr Arg Thr Gly Glu Pro Ser
36
39 Pro Pro His Asp Ile Leu His Glu Pro Pro Asp Tyr Val Ser Asp Asp
43 Glu Lys Asp His Gly Lys Lys Lys Gly Lys Phe Lys Lys Glu Lys
47 Arg Thr Glu Gly Tyr Ala Ala Phe Gln Glu Asp Ser Ser Gly Asp Glu
51 Ala Glu Ser Pro Ser Lys Met Lys Arg Ser Lys Gly Ile His Val Phe
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                                   105
55 Lys Lys Pro Ser Phe Ser Lys Lys Glu Lys Asp Phe Lys Ile Lys
                               120
59 Glu Lys Pro Lys Glu Glu Lys His Lys Glu Glu Lys His Lys Glu Glu
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63 Lys His Lys Glu Lys Lys Ser Lys Asp Leu Thr Ala Ala Asp Val Val
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75 Pro Leu Ala Asp Ala Val Glu Arg Thr Met Met Tyr Asp Gly Ile Arg
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79 Leu Pro Ala Val Phe Arg Glu Cys Ile Asp Tyr Val Glu Lys Tyr Gly
      210
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RAW SEQUENCE LISTING DATE: 01/03/2005 PATENT APPLICATION: US/10/713,578 TIME: 15:44:38

Input Set : A:\124263-1006 SEQUENCE LISTING.ST25.txt
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91	Asp	Tyr	Glu	Pro	245 Asn	Thr	Val	Ala		250 Leu	Leu	Lys	Gln	Tyr	255 Leu	Arg
	Asp	Leu	Pro	260 Glu	Asn	Leu	Leu		265 Lys	Glu	Leu	Met	Pro	270 Arg	Phe	Glu
96	<b>~1</b>	7 J -	275	<b>~</b> 1	70	ml	m1	280		~-7	_	·	285			_
100		290		GIĀ	Arg	inr	295		Thr	GIu	гàг	Va1		GIu	Phe	Gln
103	Arc	Leu	Leu	Lvs	Ara	Leu			Cvs	Asn	Tur			Tle	Ser	Trp
	305			-2	3	310		0.20	. 0,2	1101	315		шси		. DCI	320
107	Leu	Ile	Val	His	Met	Asp	His	Val	. Ile	Ala	Lys	Glu	Leu	Glu	Thr	Lys
108					325					330					335	-
111	Met	Asn	ılle	Gln	Asn	Ile	Ser	Ile	. Val	Leu	Ser	Pro	Thr	Val	Gln	Ile
112				340					345					350		
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116			355					360					365			
119	Gly	Asn	. Val	Val	Leu	Lys	Gln	. Val	Met	Lys	Pro	Leu	Arg	Trp	Ser	Asn
120		370					375					380				
			Thr	Met	Pro	Thr	Leu	Pro	Glu	Thr	Gln	Ala	Gly	Ile	Lys	Glu
	385					390					395					400
		Ile	Arg	Arg	Gln	Glu	Phe	Leu	Leu	Asn	Cys	Leu	His	Arg	Asp	Leu
128		_			405					410					415	
		Gly	Gly			Asp	Leu	Ser			Lys	Arg	Leu	Trp	Glu	Val
132		_		420		_			425					430		
		Arg			Thr	Ala	Leu			Lys	Leu	Arg		Ala	Lys	Arg
136		~3	435			_		440					445			
				Glu	Thr	ГÀЗ			Gln	Glu	Ile		Ser	Leu	Ser	Lys
140		450		<b>a</b>	Ŧ	~1	455		_		_	460				
		Asp	vaı	ser	ьys		GIu	Met	Asn	Glu		Lys	Glu	Val	Ile	
	465	Т о	T	77-	<b>~1</b>	470	7	<b>~</b> 3	~7.	-	475		~-7			480
148		ьец	ьец	Ala		GIU	Asn	GIU	тте			GIu	GIn	Glu	Glu	Leu
		מות	7 an	C1	485	Dha	T	7)	7	490		2.7	<b>a</b> .	~-3	495	
152	пец	AIa	ASII	500	GIII	Pne	ьeu	Arg	505	GIN	ше	Ala	ser		Lys	Glu
	Glu	Tla	·G111		Lou	7. ~~	7.7.	C1,,		77-	<i>α</i> 1	т1.	<b>~1</b>	510	Arg	<b>~1</b>
156	GIU	110	515	Arg	neu	Arg	Ата	520		Ald	Giu	тте		ser	Arg	GIn
	Gln	Иic		Ara	Car	Glu	Thr			Ф	Com	C 0 22	525	0	Glu	<b>a</b>
160	0111	530		n.g	Der	. Giu	535		GIU	TAT	ser	540		ser	GIU	ser
	Glu			Δen	G] 11	Glu			Gln	T1.	Tlo			7. ~~	T 0	Gln
	545	DCI	Giu	ир	GIU	550	Gru	neu	GIII	116	555	ьeu	Gru	Asp	ьец	560
		Gln	Asn	Glu	Glu		Glu	Tle	Lare	Agn		uic	T 033	7 am	Gln	
168	9		~ -~-11	JIU	565	<b></b>	oru		Ly 3	570	UOII	TITS	neu	ASII	575	нта
,	Ile	His	Glu	Glii		Glu	Δla	Tle	Tle		Len	Δνα	17 n 1	Gl n	Leu	71 200
172		0	O_u	580	9	OIU	1110	110	585	Oru	π <del>c</del> α	AT 9	vai	590	neu	Arg
	Leu	Len	Gln		Gln	Ara	Δla	Lve		Glu	Gln	Gln	λla		Glu	Λan
176			595			3	111U	600	4.1.U	Jiu	0111	CIII	605	GIII	GIU	wsb
	Glu	Glu		Glu	Trp	Arg	Gly		Ala	Val	Gln	Pro		Ara	Asp.	Gly

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180	610	•	615		620		
		u Dro Tura A		al. al. D.			-
	625		ла ята пув	Glu Gln Pro	Lys Ala Gi		
		-		635	Olas missa os	640	
188	FIO AIA Dy	645	to ser Arg	Asp Arg Lys 650	Giu inr se	655	
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	<211> LENG						
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203	tgtctgatga	tgagaaagat	catgggaaga	aaaaagggaa	atttaagaaa	aaggaaaaga	240
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				aacccaaaga			420
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VERIFICATION SUMMARY

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